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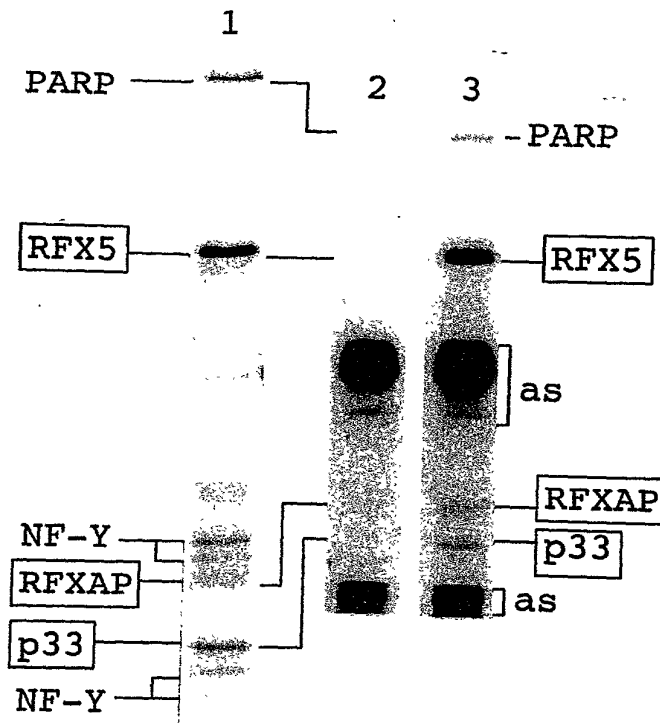


FIG. 1

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1 → 1  
ACGCAGGGAAGGAGGCACACCCGGGGTGGCGCAGTGAGGAGGGGGCGGACGGCCA  
58 GGAGGCTGGTGGAGCGACACCCAGGAGGAGGGGAAGAACTCTCTCCCTTTCTGAAC  
118 CCCCTTTCTTGAGAGCAGAGTTGGGGAGTCCTCCACGCATTACCCACTCGGGCCGCA  
178 AAAACTCCCTTCTTAGCCCTCTGCCCCCCTTGCTTATAAGCCTTTGAGACCGCAGA  
238 AGGACCTTGTGTGGAACGGGACGGCCAGAGGAAGCCAGATCGCTGAGGTCGGGTCT  
298 CCAGTTGCCTCCTGCTATATCCATTGGAAGAGAAAAGTTGTGACTTGGCCCCCAAGT  
358 TTTGAGAGAACTGGGCTTTTCGGCGGGGACAGAGGCTCGTGGGAGCTTTTCCCC  
418 ATGGAGCTTACCCAGCCTGCAGAAGACCTCATCCAGACCCAGACACCCCTGCCCTCAGAA  
1 M E L T Q P A E D L I Q T Q Q T P A S E  
478 CTTGGGACCCCTGAAGACCCCGGAGAGGCTGCAGATGGCTCAGACACTGTGTCCTC  
21 L G D P E D P G E E A A D G S D T V V L  
538 AGTCTCTTTCCCTGCACCCCTGAGCCTGTGAATCCTGAACCGGATGCCAGTGTTCCTCT  
41 S L F P C T P E P V N P E P D A S V S S  
598 CCACAGGcagGCAGCTCCCTGAAGCACTCCACCACTCTCACCAACCGGACGAGGGAAC  
61 P Q (A) G S S L K H S T T L T N R Q R G N

FIG. 2A

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658 GAGGTGTCAGCTCTGCCGGCCACCCTAGACTCCCTGTCCATCCACGAGCTCGCAGCACAG  
 81 E V S A L P A T L D S L S I H Q L A A Q  
 718 GGGAGCTGGACCAGCTGAAGGAGCATTTGCGGAAAGGTGACAACTCGTCAACAAGCCA  
 101 G E L D Q L K E H L R K G D N L V N K P  
 778 GACGAGCGGGCTTCACCCCCCTCATCTGGGCCCTCCGCCCTTTGGAGAGATTGAGACCGTT  
 121 D E R G F T P L I W A S A F G E I E T V  
 838 CGCTTCCTGCTGGAGTGGGTGCCGACCCACATCCTGGCAAAGAGCGAGAGCGGCC  
 141 R F L L E W G A D P H I L A K E R E S A  
 898 CTGTCGCTGGCCAGCACAGCGGGCTACACAGACATTGTGGGGCTGCTGGAGCGGTGAC  
 161 L S L A S T G G Y T D I V G L L L E R D  
 958 GTGGACATCAACATCTATGATTGGAATGGAGGACGCCACTGCTGTACGCTGTGCGCGGG  
 181 V D I N I Y D W N G G T P L L Y A V R G  
 1018 AACCACGTGAAATGCGTTGAGGCCTTGCTGGCCCGAGGCGCTGACCTCACCACCGAAGCC  
 201 N H V K C V E A L L A R G A D L T T E A  
 1078 GACTCTGGCTACACCCCGATGGACCTTGCCGTGGCCCTGGGATACCGGAAAGTGCAACAG  
 221 D S G Y T P M D L A V A L G Y R K V Q Q

FIG. 2B

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1138 GTGATCGAGAACCATCTCAAGCTCTTCAGAGCAACCTGGTGCCCGCTGACCCCTGAG  
241 V I E N H I L K L F Q S N L V P A D P E  
1198 TGAAGGCCGCTGCCGGGACTCAGACACTCAGGGAACAAAATGGTCAGCCAGAGCTGGG  
260 \*  
1258 GAAACCCAGAACTGACTTCAAAGGCAGCTTCTGGACAGGTGGTGGGAGGGACCCCTTCCC  
1318 AAGAGAACCAATAAACCTTCTGTGCAG - polyA

FIG. 2C

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HsREFXANK	MELTQPAEDLIQTQTFASELGDPEDPGEEAAGSDTVVLSLFCTPEPVNPEPDASVSS	60
MmREFXANK	--P--V--N--VPN--P--VPD-E---TRD-SPEN	60
Hs homol	NAFNVETEVFHLAECNIHTSPSPGIGVHRHVXTP-T	35
Mm homol	ASVLFKAECNIHTSPSPGIGVHRHVYTP-T	29
HsREFXANK	HHHHT HHHHHHHHHHT	
MmREFXANK	PQaGSSSLKHSTLTNRQRGNEVSALPATLDSLSIHQLAAQGELDQLKEHLRKG.....	113
Hs homol	L--F-----S--D--acpactc	119
Mm homol	TKHF-PI-Q-----KH-----TT-LLAN--V-----MLY-ATRIEQ.....	87
GABPβ	TKHF-PI-Q-----KH-----TT-LLAN--A-----MLY-ATRIEQ.....	81
	EA-RA-QD-EVRILMAN-.....	25
HsREFXANK	ank 1	
MmREFXANK	TT HHHHHHHHT HHHHHHHHTTT TT TT HHHHHHHHT H	
Hs homol	...DNLVNKPDERGETPLIWASAFGEIETVRFLEWGADPHILAKERESALSTGGYT	170
Mm homol	lsgN--I-----D-----M-----	179
GABPβ	...E-VI-HT--E-----M--A-H-Q-AV-E--QN-----QL-G-G-----CSK---	144
	...E-VI-HT--E-----M--A-H-Q-AV-E--QN-----QL-G-G-----CSK---	138
	...APFTT..-WL-TS--HL-AQY-HFS-TEV--RA-VSRDART-VDRTTP-HM-ASE-HA	80

FIG. 3A

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	ank 2	ank 3	
HsREFXANK	HHHHHHHTT TT TTT HHHHHHHHTT	HHHHHHHHHTT TT TTT HHHHH	
MmREFXANK	DIVGLLLERDVVDINIYDWMNGTPLLAVRGNHVKCVALLARGADLTTEADSGYTPMDLA		230
Hs homol	---R---D---		239
Mm homol	---XM---DCG---V-X---	---H---	204
GABPβ	---KM---DCG---V-E---	---GH---	198
	N---EV---KHGA-V-AK-MLKM-A-HW-TEH---QEV---L-IKY---VH-QSKECK-AF-IS	---KM---ES---P-I-T---NS---	140
		---KM---EN---P-I-T---NS---	

HsREFXANK	HHTT HHHHHHH	
MmREFXANK	VALGYRKVQQVIENHILKLFQSNLVPADPE	260
Hs homol	-----M-S---R-----T-G-V---	269
Mm homol	-----IEVFNRLLSHIC	220
GABPβ	-----GCSDYMLVTDVERI	218
	IDN-NEDLAEILQ	153

FIG. 3B

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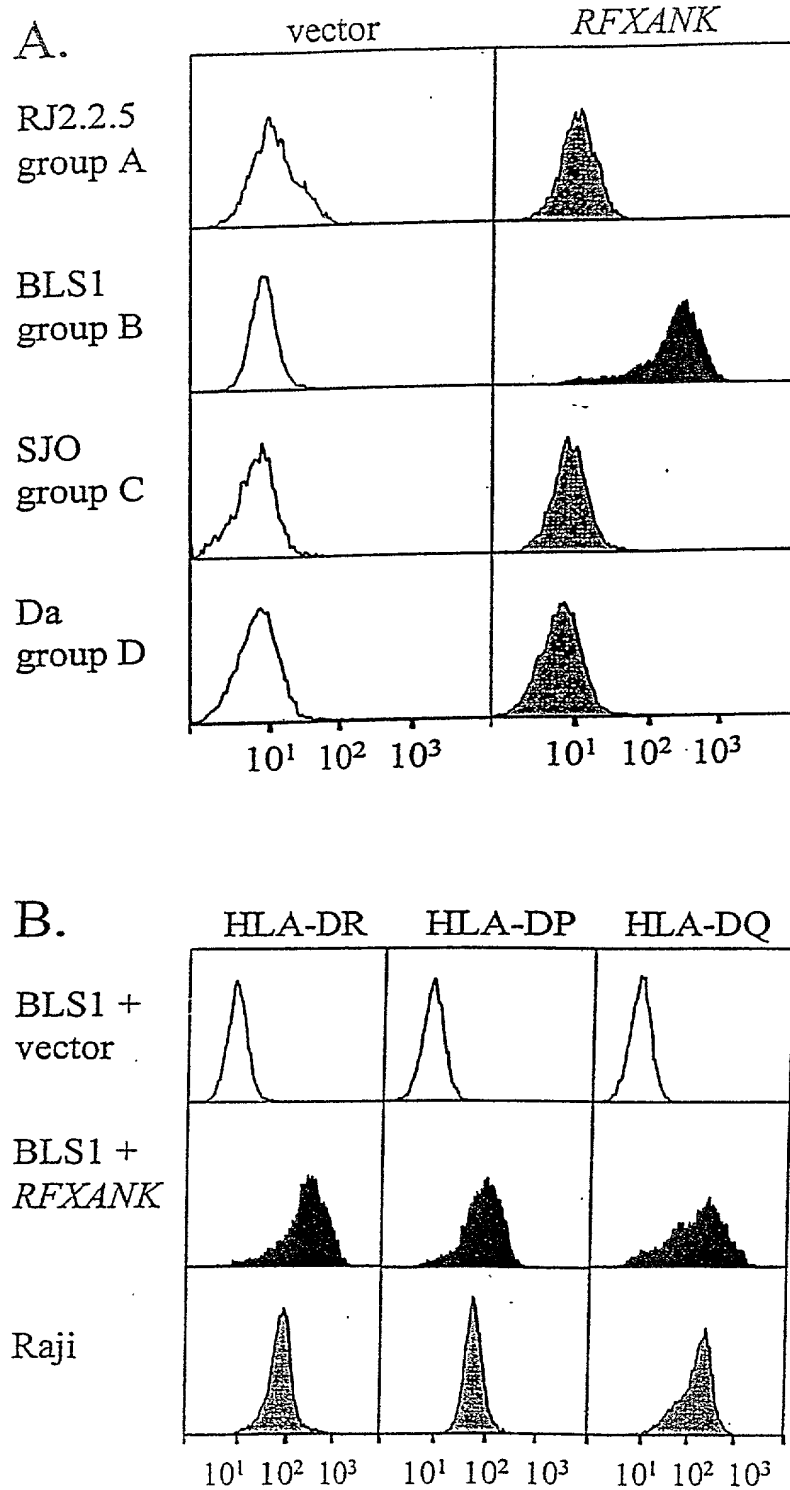


FIG. 4

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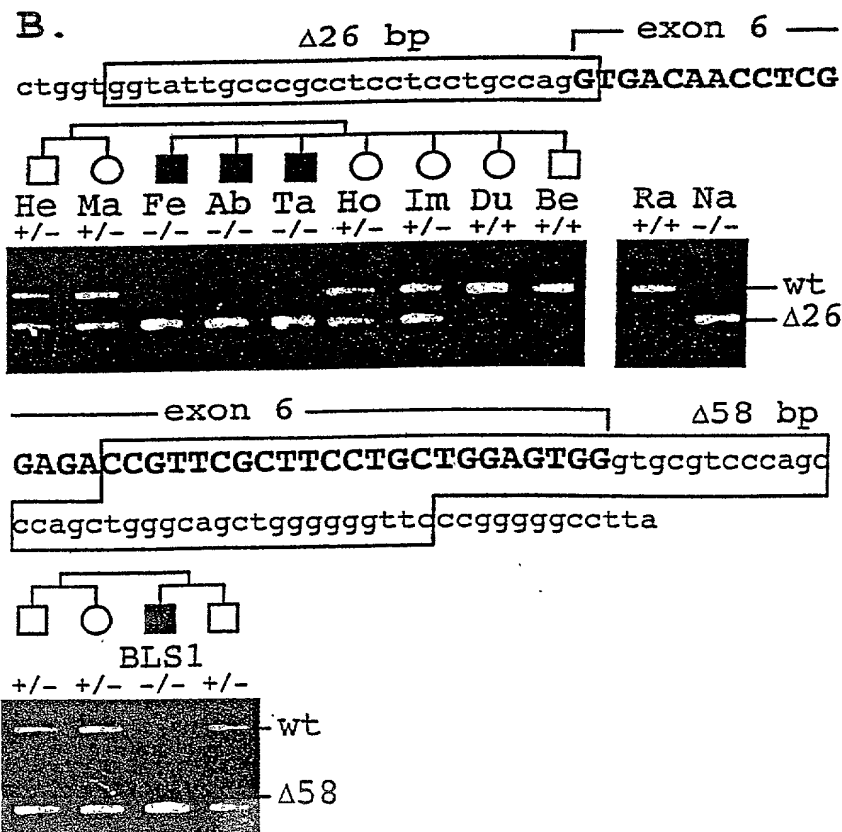
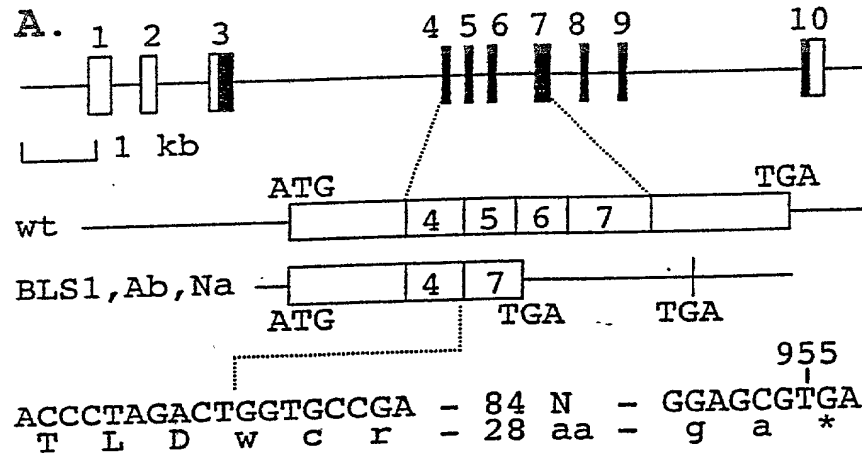
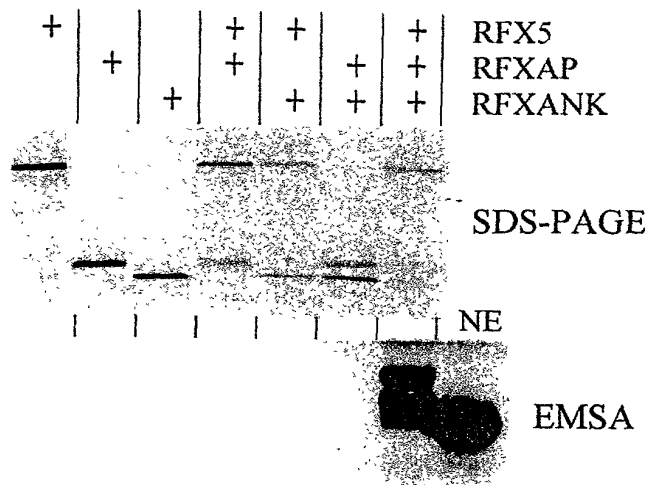


FIG. 5



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**A.**



**B.**

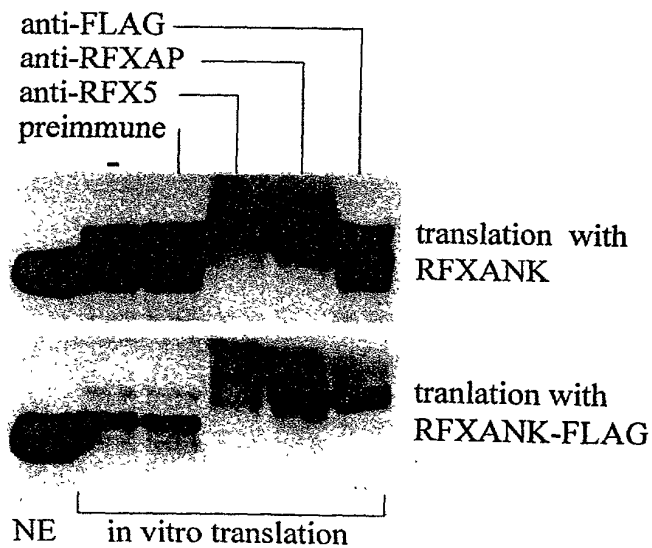


FIG. 6

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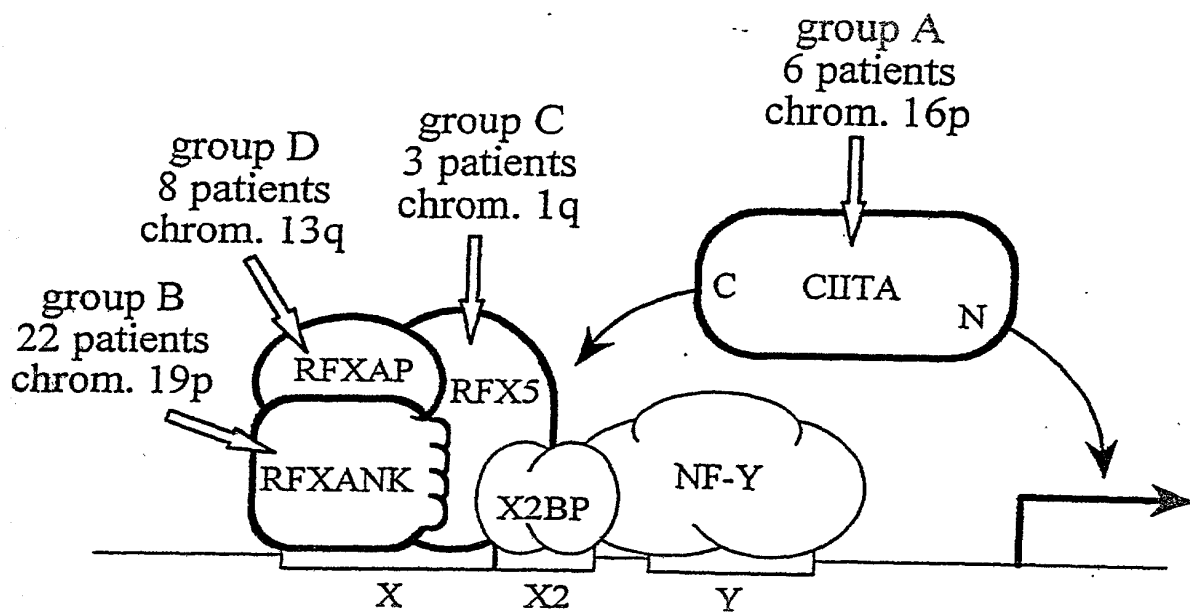


FIG. 7

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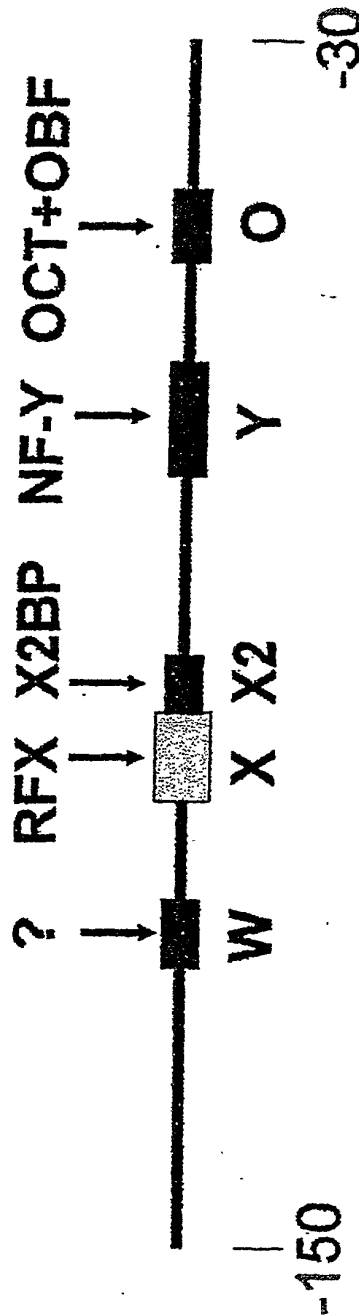


FIG. 8

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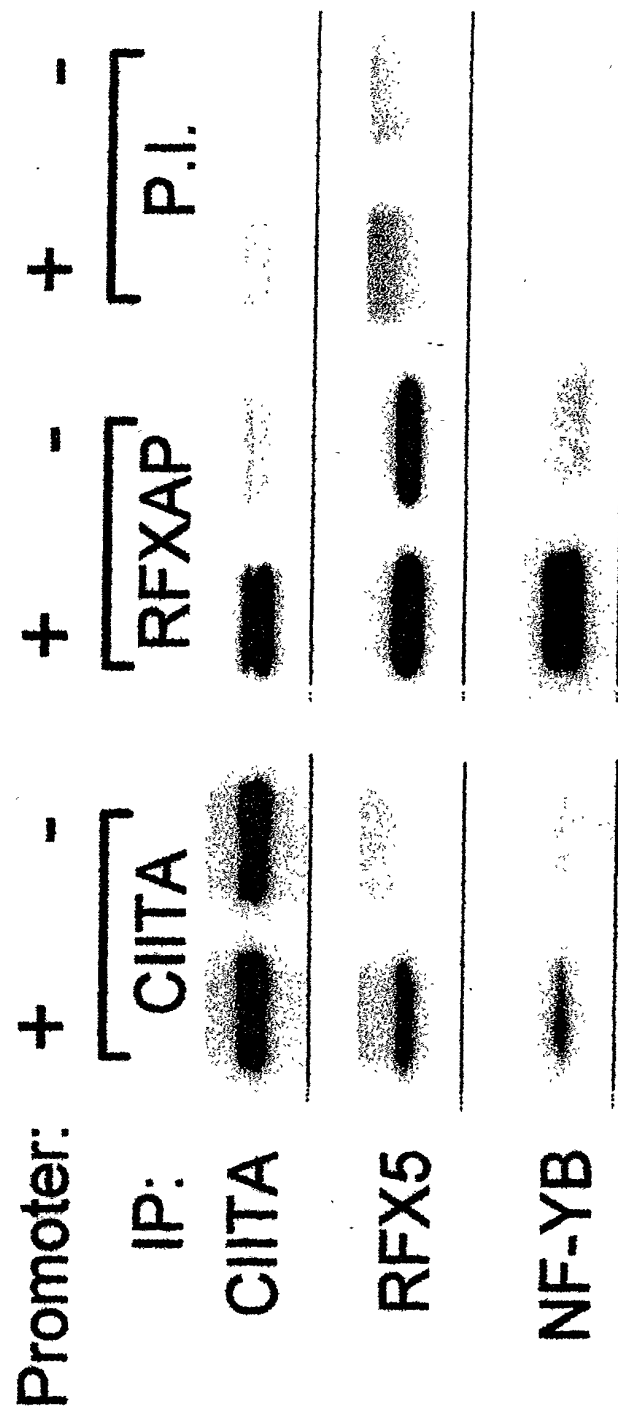


FIG. 9

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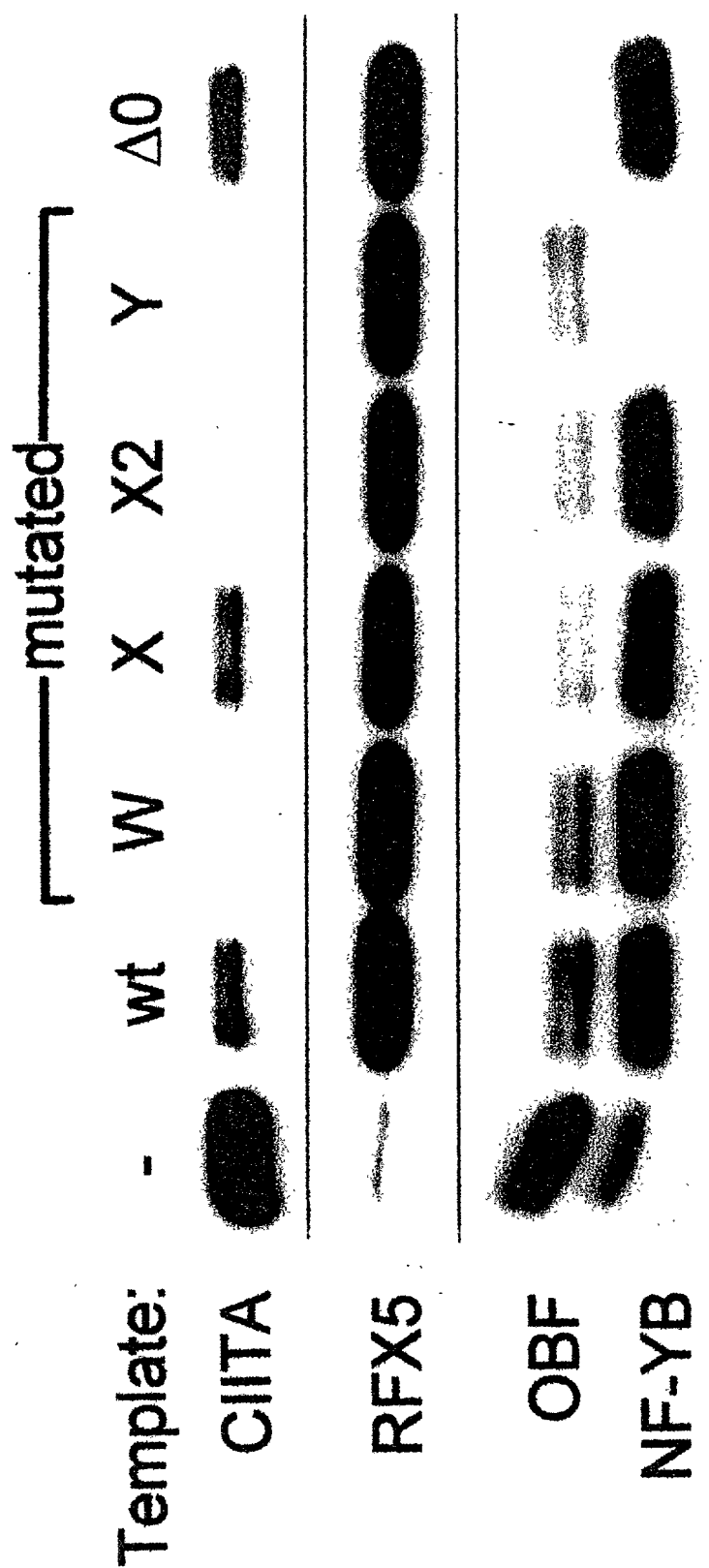


FIG. 10A

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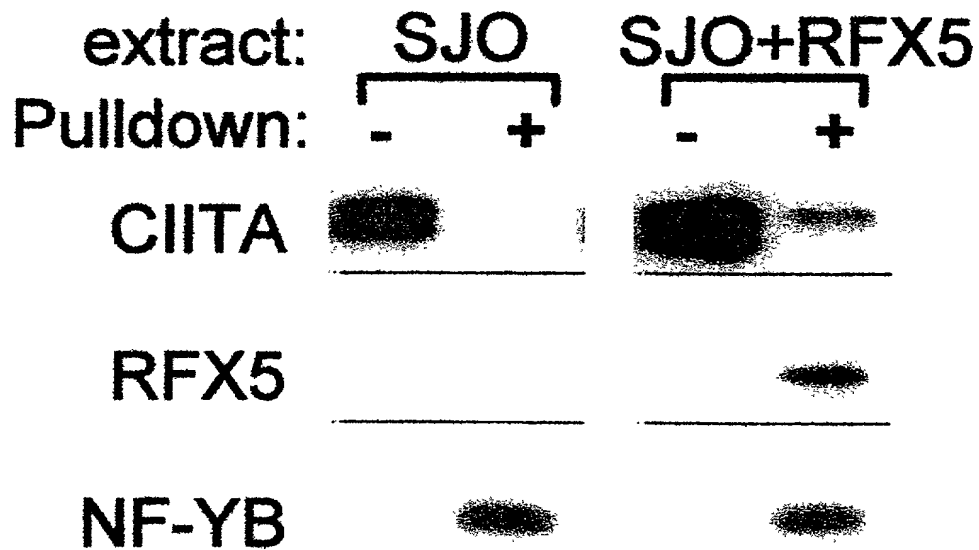


FIG. 10B

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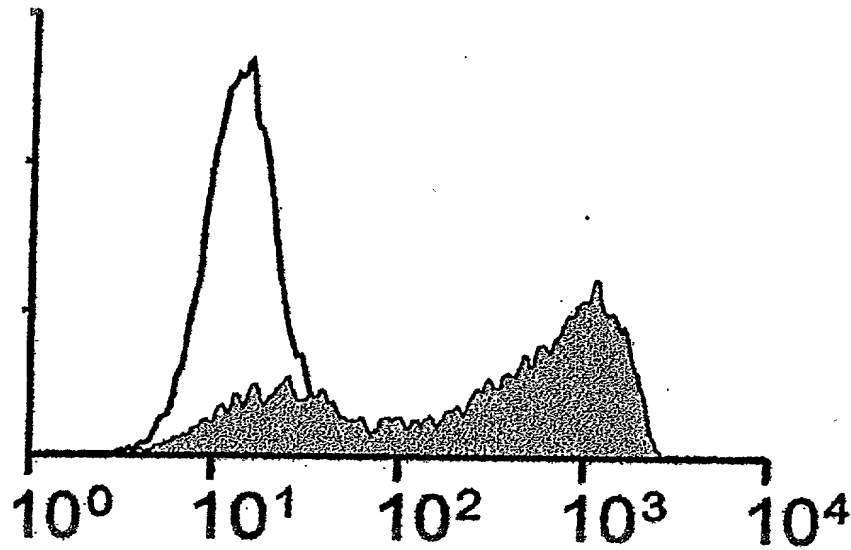


FIG. 10C

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FIG. 11A



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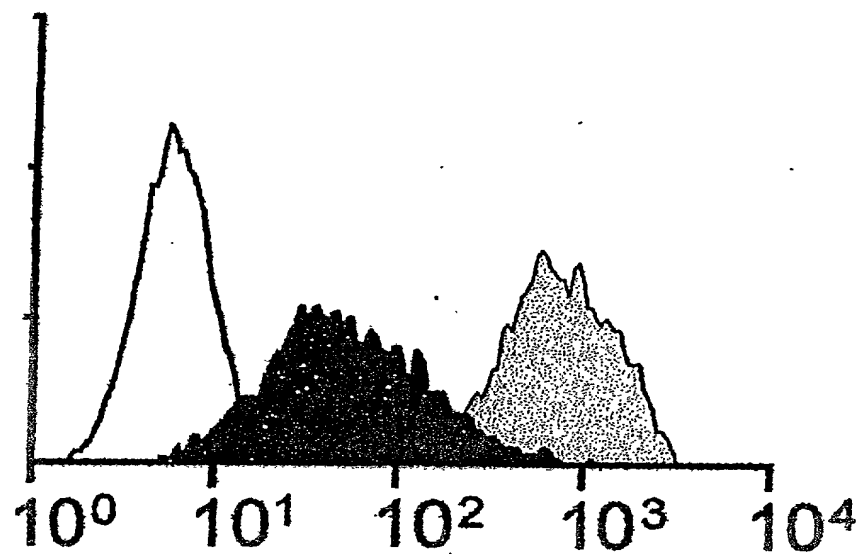


FIG. 11B

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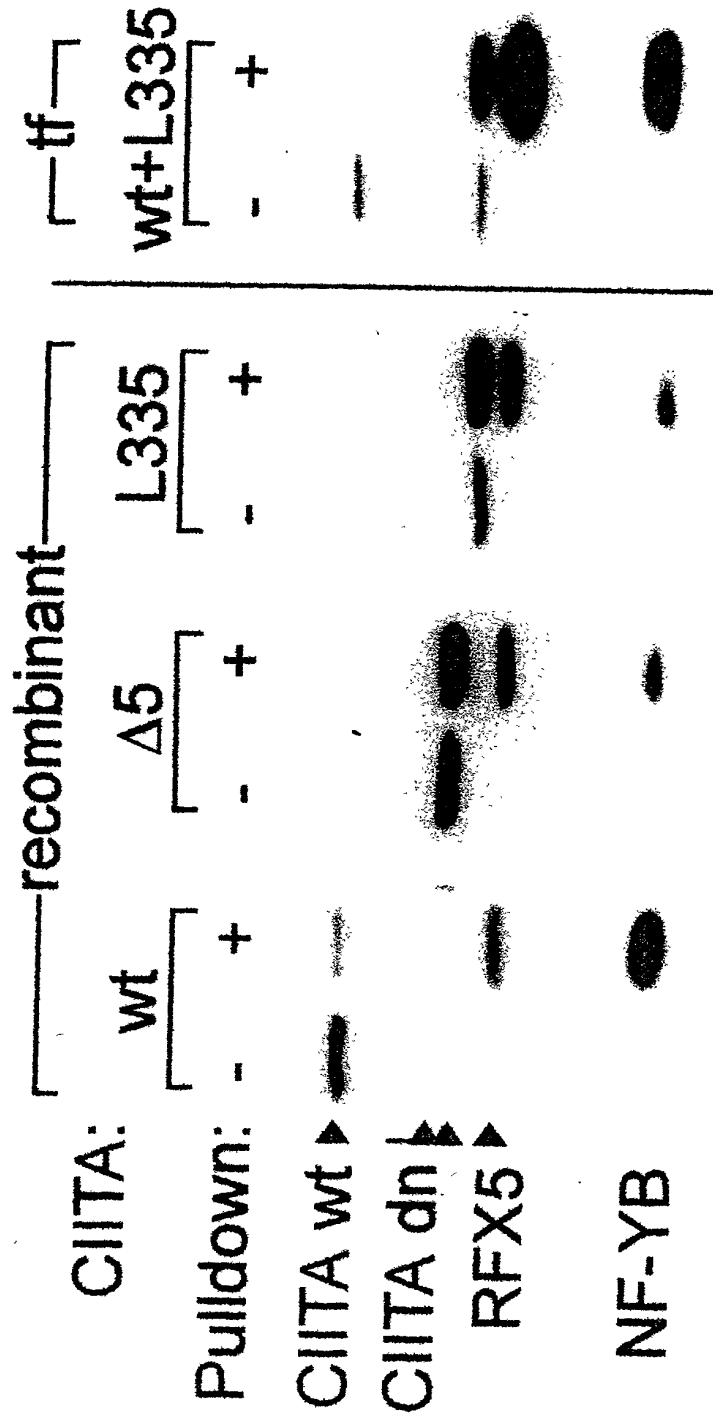


FIG. 11C

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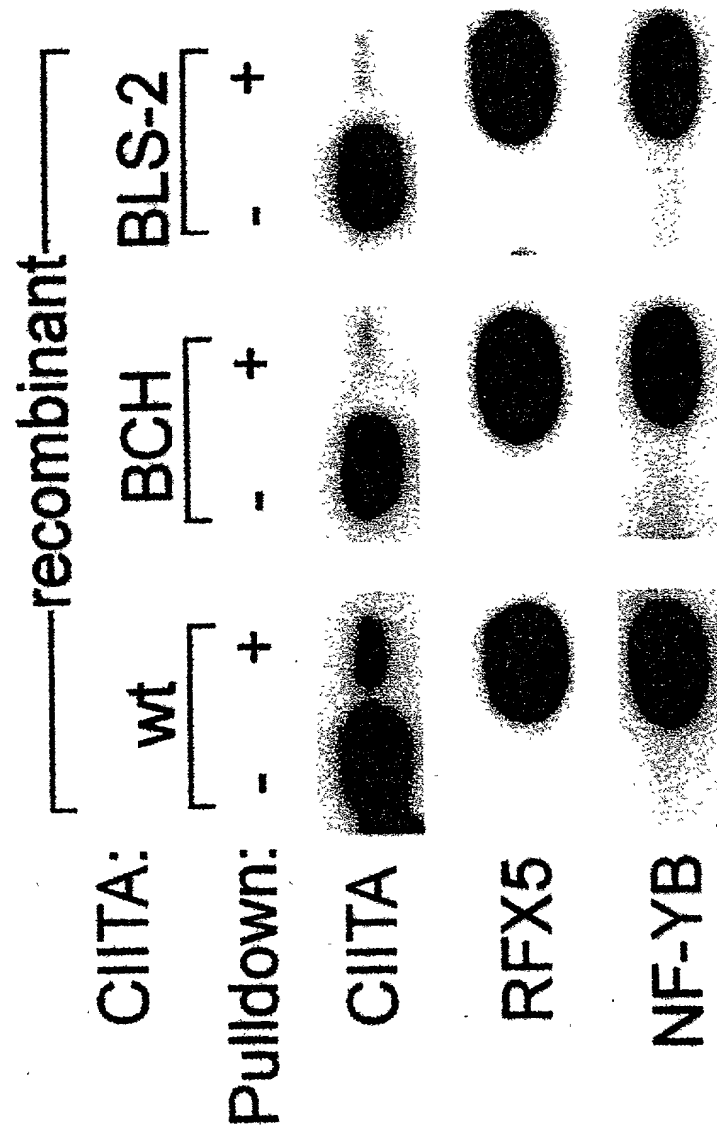


FIG. 11D